IN THE CLAIMS

This listing of the claims replaces all prior versions of the claims in the application.

Claims 1-2 (canceled)

Claim 3. (Previously presented) An isolated polynucleotide encoding a polypeptide selected from the group consisting of:

a.) a polypeptide comprising the amino acid sequence of SEQ ID NO:1,

b) a polypeptide comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:1,

c) a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:1, said fragment having cyclic nucleotide phosphodiesterase activity, and

d) an immunogenic fragment of a polypeptide of at least 5 amino acids of the amino acid sequence of SEQ ID NO:1, said immunogenic fragment is used to make an antibody which specifically binds to an isolated polypeptide selected from the group consisting of a), b) and c).

Claims 4-5 (canceled)

Claim 6. (Original) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

Claim 7. (Original) A cell transformed with a recombinant polynucleotide of claim 6.

Claim 8. (Previously presented) A method for producing a polypeptide encoded by the polynucleotide of claim 3, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 3, and

b) recovering the polypeptide so expressed.

Claims 9-10 (canceled)

Claim 11. (Previously presented) An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:2,

b) a polynucleotide comprising a polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:2,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b) and

e) an RNA equivalent of a)-d).

Claim 12 (canceled)

Claim 13. (Original) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

Claim 14. (Original) A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

Claim 15. (Original) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

Claims 16-19 (canceled)

Claim 20. (Withdrawn) A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 53, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

Claim 21. (Original) A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

Claims 22-49 (canceled)

Claims 50-51 (Not entered)

Claim 52. (Previously presented) A method of claim 8, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:1.

Claim 53. (Previously presented) A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:2.